

## REVIEW

# The role of ATP-sensitive potassium channels in cellular function and protection in the cardiovascular system

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ATP-sensitive potassium channels ( $K_{ATP}$ ) are widely distributed and present in a number of tissues including muscle, pancreatic beta cells and the brain. Their activity is regulated by adenine nucleotides, characteristically being activated by falling ATP and rising ADP levels. Thus, they link cellular metabolism with membrane excitability. Recent studies using genetically modified mice and genomic studies in patients have implicated  $K_{ATP}$  channels in a number of physiological and pathological processes. In this review, we focus on their role in cellular function and protection particularly in the cardiovascular system.

### Abbreviations

ABC, ATP binding cassette; AP, action potential;  $K_{ATP}$ , ATP-sensitive potassium channel;  $K_{CO}$ , ATP-sensitive potassium channel opening drug;  $PIP_2$ , phosphatidyl 4,5-bisphosphate; SUR, sulphonylurea receptor; VSM, vascular smooth muscle

## Introduction

Two independent laboratories can lay claim to having first described the ATP-sensitive potassium channels ( $K_{ATP}$ ; channel nomenclature follows Alexander *et al.*, 2013). Noma (1983) observed the appearance of an outward  $K^+$  current in heart muscle cells when treated with metabolic poisons or hypoxia. This was reversed by ATP injected into the cell. Similar observations were made by another group (Trube and Hescheler, 1984). Such channels were subsequently described in pancreatic beta cells (Ashcroft *et al.*, 1984), skeletal muscle (Spruce *et al.*, 1985), smooth muscle (Standen *et al.*, 1989) and neurones (Ashford *et al.*, 1988). During this period, the basic electrophysiological and pharmacological properties of the channel were elucidated (Ashcroft, 1988; Noma and Takano, 1991). In inside-out patches in ~140 mM symmetrical  $K^+$  concentrations, the single-channel conductance is ohmic with a conductance of 70–80 pS. The lower values sometimes noted in the literature generally have lower and asymmetric  $K^+$  concentrations. The channel is highly selective for potassium ( $P_{Na}/P_K \sim 0.01$ ). Activity is inhibited by the application of ATP with a  $K_i$  of 10–500  $\mu$ M with a Hill coefficient of more than 1 (generally around 2) depending on the

tissue and recording configuration. The ATP inhibition is not dependent on ATP hydrolysis: it is not reliant on  $Mg^{2+}$  and ATP can be substituted by non-hydrolysable derivatives. In the absence of magnesium other adenine nucleotides can inhibit channel activity but they are less potent. However, in the presence of  $Mg^{2+}$  and ATP, ADP is stimulatory.

Even at the beginning of the 1990s the channels were known to have a rich pharmacology (see Edwards and Weston, 1993). Sulphonylureas were discovered accidentally when it was noted that the anti-microbial sulphonamides caused hypoglycaemia in animals. It became apparent that stimulation of insulin release from pancreatic beta cells occurred because of inhibition of  $K_{ATP}$  channels. There is a family of these drugs: the most widely known are the first-generation agents (e.g. tolbutamide, chlorpropamide) and the more potent second-generation agents (e.g. glibenclamide, gliclazide, glipizide). These agents still have a place in the management of type 2 diabetes mellitus. There are also agents that are able to open  $K_{ATP}$  channels [ $K_{ATP}$  channel opening drugs ( $K_{CO}$ s)]. Intriguingly, not only are some of these agents selective for  $K_{ATP}$  but they also exhibit a very broad range of chemical structures: for example, diazoxide is a benzothiadiazine, pinacidil a cyanoguanidine and

nicorandil a pyridyl nitrate (Mannhold, 2006). Agents known to block other K<sup>+</sup> channels, for example, Ba<sup>2+</sup> and 4-aminopyridine, are also active on K<sub>ATP</sub> channels.

## Molecular cloning

The inwardly rectifying family of potassium channels (K<sub>IR</sub>) resisted cloning even after the elucidation of the primary structure of voltage-gated potassium channels. It was not until expression cloning techniques were employed that the first cDNAs were isolated (Ho *et al.*, 1993; Kubo *et al.*, 1993) and a substantial gene family with seven subfamilies was revealed (see Nichols and Lopatin, 1997). The pore-forming  $\alpha$  subunits have two transmembrane domains with an intracellular N- and C-terminus. The only significant area of homology with the voltage-gated family was the pore-forming H5 segment responsible for potassium selectivity. Initially, however, homology cloning approaches did not elucidate an obvious candidate for the K<sub>ATP</sub> channel that functioned as expected in a heterologous expression system. A critical missing component was revealed as the sulphonylurea receptor (SUR) (Aguilar Bryan *et al.*, 1995). Co-expression of the K<sub>IR</sub>6.0 family of inwardly rectifying potassium channels with the SUR reconstituted the K<sub>ATP</sub> channel (Inagaki *et al.*, 1995a,c). It became apparent that there were two isoforms of K<sub>IR</sub>6.0 (K<sub>IR</sub>6.1 and K<sub>IR</sub>6.2) and two variants of SUR (SUR1 and SUR2 with two splice variants SUR2A and SUR2B) (Inagaki *et al.*, 1996; Isomoto *et al.*, 1996; Yamada *et al.*, 1997). SUR is a member of the ATP-binding cassette (ABC) family of protein (Linton and Higgins, 2007). It is most closely related to the multidrug resistant-related proteins and they are now all classified in the ABCC family (Toyoda *et al.*, 2008). Characteristically, SUR has 17 transmembrane segments grouped into three domains comprised of five (TMD0), six (TMD1) and six (TMD2) helices respectively. The N-terminus is extracellular and each of these domains is connected by intracellular linkers and finally an intracellular C-terminus. The TMD1-TMD2 and C-terminus contain nucleotide-binding domains (NBDs) with Walker A and Walker B motifs and linker regions indicative of ATP binding and hydrolysis (Linton and Higgins, 2007). This topology is well supported by experimental data (Conti *et al.*, 2001). At the genomic level, the genes encoding SUR1 and K<sub>IR</sub>6.2 and SUR2 and K<sub>IR</sub>6.1 are adjacent to one another on 11p15.1 and 12p12.1, respectively, and this arrangement suggests a coordinated regulation of the SUR and K<sub>IR</sub>6.0 subunit (Inagaki *et al.*, 1995a,b; Chutkow *et al.*, 1996). The mature K<sub>ATP</sub> channel complex is a hetero-octamer of four K<sub>IR</sub>6.0 subunits and four SUR subunits (Clement *et al.*, 1997; Shyng and Nichols, 1997). A diagram of K<sub>ATP</sub> channel assembly is shown in Figure 1.

SUR2A\K<sub>IR</sub>6.2 underlies the cardiac K<sub>ATP</sub> channel present in ventricular muscle and SUR2B\K<sub>IR</sub>6.1 that in smooth muscle. However, there are qualifications to this simplified picture. K<sub>IR</sub>6.1 is ubiquitously expressed and thus there exists the potential for heteromultimerization with K<sub>IR</sub>6.2. Indeed, this can be demonstrated with heterologous expression (Cui *et al.*, 2001) and it might occur potentially in the cardiac conduction system (Yoshida *et al.*, 2004; Bao *et al.*, 2011b). The issue of whether different SUR subunits can heteromultimerize is more controversial but practically there are not

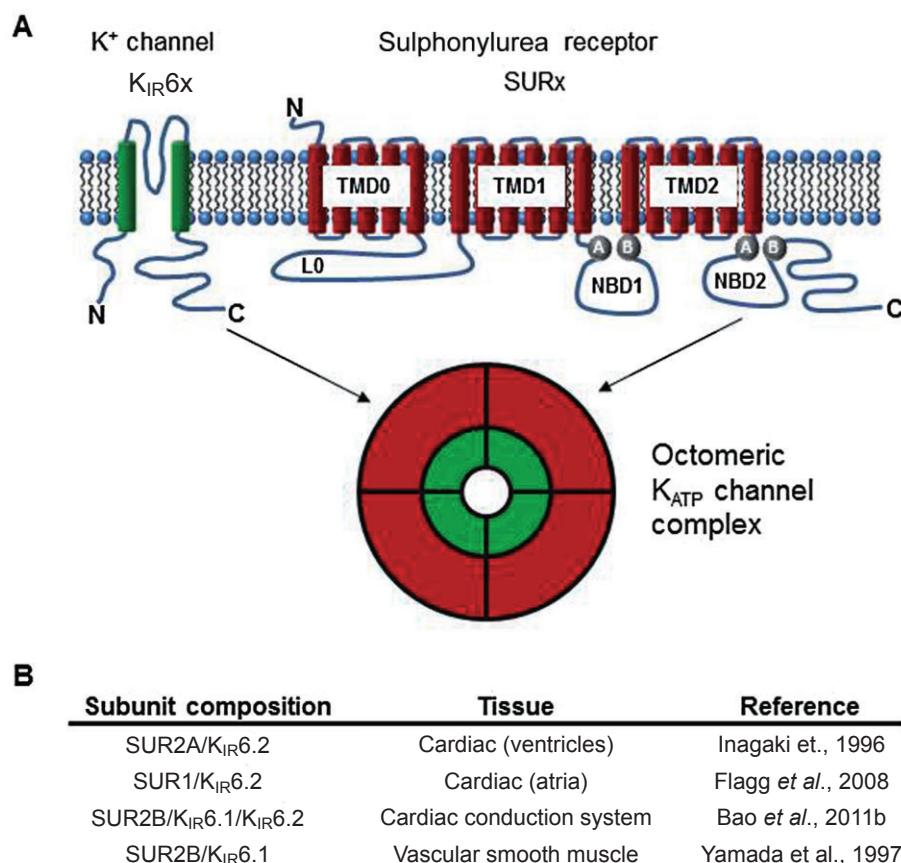
many occasions where more than one isoform is expressed and the evidence favours homomultimers (Giblin *et al.*, 2002; Tricarico *et al.*, 2006; Cheng *et al.*, 2008). Secondly, the composition of the channels may show subtle but important anatomical variations. For example, K<sub>ATP</sub> in atrial cardiac myocytes is constituted by SUR1\K<sub>IR</sub>6.2 and this differential tissue distribution may open the door for selective pharmacological manipulation in the heart in atrial fibrillation (Flagg *et al.*, 2008). Finally, most smooth muscle K<sub>ATP</sub> channels have been known to be functionally different for some time. Some of these channels have a lower single-channel conductance (~35 pS), an absolute dependence on the provision of nucleotide diphosphates for activity ('K<sub>NDP</sub>') and are less sensitive to ATP inhibition (Beech *et al.*, 1993). These properties were reproduced by the co-expression of SUR2B and K<sub>IR</sub>6.1 subunits in heterologous systems (Yamada *et al.*, 1997; Cui *et al.*, 2002). However, K<sub>IR</sub>6.2 alone or together with K<sub>IR</sub>6.1 and SUR2B might participate in some vascular beds and in non-vascular smooth muscle (Teramoto *et al.*, 2009).

The octameric nature of the channel complex has led to interesting structure-function questions. This area has been reviewed extensively (Rodrigo and Standen, 2005; Flagg *et al.*, 2010). The continuing crystallization of K<sup>+</sup> channels is likely to enrich and supersede much of this work. A high resolution structure of the K<sub>ATP</sub> channel complex or that of the K<sub>IR</sub>6.0 pore-forming subunit alone has not yet been reported. A low resolution cryoEM study was possible and showed a compact structure with the four SUR1 subunits interacting with K<sub>IR</sub>6.0 in the cytosolic and membrane domains (Mikhailov *et al.*, 2005). One interesting feature was a cleft between the SUR1 subunits by which ATP could access its binding site. The crystal structure of K<sub>IR</sub>2.2, with and without phosphatidyl 4,5-bisphosphate (PIP<sub>2</sub>), offers insight into potential gating mechanisms that might be revealed by high-resolution K<sub>ATP</sub> channel structures (Hansen *et al.*, 2011). The most recent structure of the K<sub>IR</sub>3.0 family of channels shows that these channels possess two gates, one as described for K<sub>IR</sub>2.2 and another in the C-terminus, potentially gated by G-protein  $\beta$  subunits. Both gates need to be open to exhibit channel activity (Whorton and MacKinnon, 2011).

## Metabolic regulation and mitochondrial K<sub>ATP</sub> channels

One of the defining features of K<sub>ATP</sub> channels is their sensitivity to metabolic changes. The inhibition by ATP is determined by the K<sub>IR</sub>6.0 subunit and site-directed mutagenesis has identified key residues in the C- and N-terminus of the K<sub>IR</sub>6.2, in particular R50, C166, I167, T171 and K185 (Tucker *et al.*, 1997; 1998), and this work underpins a detailed structural model (Antcliff *et al.*, 2005). K<sub>IR</sub>6.1 may also have more substantial ATP sensitivity than is generally appreciated (Babenko and Bryan, 2001), though it may depend on the recording configuration and cellular environment (Cui *et al.*, 2002). It is certainly true that both K<sub>IR</sub>6.1 and K<sub>IR</sub>6.2 containing channel complexes are sensitive to metabolic poisoning (Farzaneh and Tinker, 2008).

The issue of how SUR interacts with nucleotides is complex and not fully resolved. Early work showed that the SUR subunit endows the channel complex with sensitivity to



## Figure 1

Molecular basis of the K<sub>ATP</sub> channel. (A) K<sub>ATP</sub> channels are composed of K<sub>IR</sub>6x (6.1 or 6.2) and SUR subunits. A tetrameric arrangement of K<sub>IR</sub>6x subunits forms the channel pore, with each subunit comprised of two transmembrane domains (M1 and M2) with intracellular N- and C-terminus and a pore-forming H5 region with the K<sup>+</sup> selectivity sequence. SUR has 17 transmembrane segments split into three domains, TMD0-2. TMD0 and L0 interact and modulate gating of K<sub>IR</sub>6. TMD1-2 and the C-terminus contain the NBD1 and NBD2 with Walker A and B motifs where ATP binding and hydrolysis take place. SUR is also the pharmacological target of K<sub>CO</sub> compounds such as pinacidil and diazoxide, and sulphonylurea drugs, such as glibenclamide and tolbutamide. The mature K<sub>ATP</sub> channel is a hetero-octameric structure of K<sub>IR</sub>6x and SURx subunits. (B) Tissue-specific composition of K<sub>ATP</sub> channels in the cardiovascular system.

activation by MgADP, and this is a function of the NBDs (Gribble et al., 1997; Shyng et al., 1997). NBDs are asymmetric in function with NBD2 binding and hydrolysing MgATP rapidly while NBD1 binds ATP even in the absence of Mg<sup>2+</sup> and hydrolyses it more slowly (Ueda et al., 1997; Bienengraeber et al., 2000). Furthermore, experiments using vanadate and beryllium which mimic the post- and pre-hydrolytic states, respectively, support the idea that ATP hydrolysis at NBD2 is needed for channel activation (Zingman et al., 2001). However, in inside-out patches, MgADP potentially activates the channel, suggesting the activated state is directly accessible without prior hydrolysis. More recent work supports the idea that hydrolysis at NBD2 may not be necessary for activation (Ortiz et al., 2013). Another feature that has not been resolved is the potential dimerization of the NBDs during this cycle. In other ABC transporters, dimerization is a necessary prerequisite for ATP hydrolysis (Linton and Higgins, 2007). Thus, there are some outstanding questions in this complex mechanism. In the intact cell, studies have revealed the interaction of K<sub>ATP</sub> channels with enzymes involved in cell metabolism. The cardiac

channel complex (K<sub>IR</sub>6.2/SUR2A) is able to directly interact with adenylate kinase, creatinine kinase and lactate dehydrogenase (Carrasco et al., 2001; Crawford et al., 2002a,b). These interactions may make the channel sensitive to small changes in cytoplasmic ATP within the cell and to ATP derived from glycolysis (Weiss and Lamp, 1987).

There have been suggestions that K<sub>ATP</sub> channels are also present in mitochondria ('mitoK<sub>ATP</sub>') (Inoue et al., 1991; Paucek et al., 1992). In the first study, channel activity was directly assayed to demonstrate a 10 pS channel inhibited by ATP and glibenclamide. Subsequent work revealed a possibly unique pharmacology in that mitoK<sub>ATP</sub> was inhibited by 5-hydroxydecanoate and activated by diazoxide, properties not shared by the cardiac sarcolemmal channel (Grover and Garlid, 2000). However, these distinguishing features are no longer so clear cut (Li et al., 2010). The most convincing approach would be to directly clone the subunits. Are the known K<sub>IR</sub>6.0 and/or SUR subunits the molecular equivalent of mitoK<sub>ATP</sub>? A number of studies have proposed that K<sub>IR</sub>6.1 might be a mitoK<sub>ATP</sub> subunit specifically showing a mitochondrial localization or comparable pharmacology (Suzuki et al.,

1997; Liu *et al.*, 2001); however, the commercial antibodies may be detecting other unrelated proteins in mitochondria (Foster *et al.*, 2008). If K<sub>IR</sub>6.1 does not underlie mitoK<sub>ATP</sub> channels what are the other possibilities? One group isolated a complex of a succinate dehydrogenase, mitochondrial ABC protein 1, phosphate carrier, adenine nucleotide translocator and ATP synthase (Ardehali *et al.*, 2004). However, none of these proteins contain the canonical elements in the H5 segment of the established potassium channels and structures. Furthermore, some of the drugs used seem to have effects or are metabolized in other pathways (Das *et al.*, 2003; Hanley *et al.*, 2005). The most recent work in this area may address some of these issues (Foster *et al.*, 2012). These authors isolated K<sub>IR</sub>1.2 from the inner mitochondrial membranes of bovine heart and cell imaging confirmed the mitochondrial localization of K<sub>IR</sub>1.2, albeit after heterologous expression. In pharmacological studies, overexpression of K<sub>IR</sub>1.2 along with the use of shRNA to silence the protein, implicated this channel subunit as underlying mitoK<sub>ATP</sub> and having a role in cellular protection. These are potentially exciting findings but await confirmation and validation using more *in vivo* approaches.

## Regulation through cell signalling pathways

K<sub>ATP</sub> channels have a tendency to run down in ATP-free solutions and the channel activity can be 'refreshed' with low concentrations of MgATP. This dependence was not understood until channel activity was shown to be absolutely dependent on membrane phosphoinositides, in particular PIP<sub>2</sub> (Hilgemann and Ball, 1996; Fan and Makielski, 1997; Shyng and Nichols, 1998). The ATP is needed for the synthesis of plasma membrane PIP<sub>2</sub> via PI kinases and the PIP<sub>2</sub> antagonizes ATP inhibition and leads to channel opening (Shyng and Nichols, 1998; Pratt *et al.*, 2011). Direct evidence for the involvement of membrane PIP<sub>2</sub> has been obtained using an elegant binary membrane recruitment system and this works for K<sub>ATP</sub> channel regulation also (Suh *et al.*, 2006; Quinn *et al.*, 2008). There is likely to be a direct interaction with the protein as the channel, K<sub>IR</sub>2.1 and K<sub>IR</sub>2.2 in this case, can be purified and reconstituted in liposomes of fixed lipid composition (D'Avanzo *et al.*, 2010). Furthermore, recent crystal structures show PIP<sub>2</sub> binding in the homologous K<sub>IR</sub>2.2 leads to C-terminal domain translocation to interact with the transmembrane domain and this change opens the helix bundle gate which occludes the lower pore.

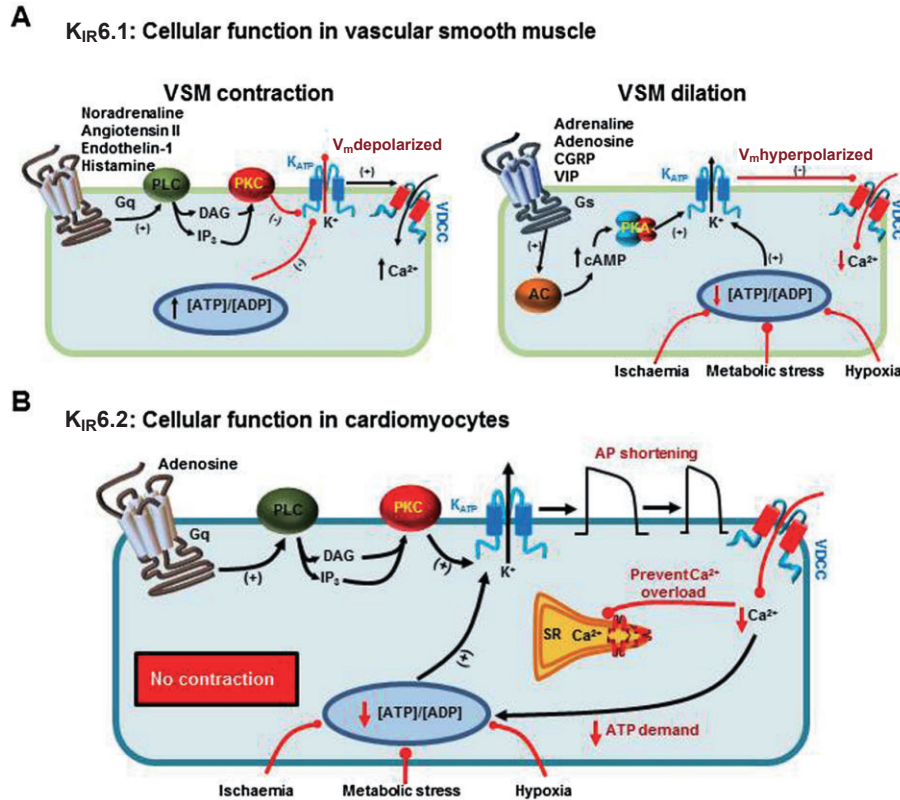
In smooth muscle, downstream activation of PKA through various receptors coupled to the stimulatory G-protein G<sub>s</sub>, such as adenosine A<sub>2</sub>, β adrenoreceptors, calcitonin gene-related peptide and prostacyclin, leads to vasodilatation. A major contribution to the vascular smooth muscle (VSM) cell hyperpolarization is the opening of K<sub>ATP</sub> channels (Standen *et al.*, 1989; Nelson *et al.*, 1990; Rodrigo and Standen, 2005). Subsequent molecular studies on K<sub>IR</sub>6.1/SUR2B revealed that this was likely due to the direct phosphorylation of both channel subunits (T633, S1387 and S1465 on SUR2B; S385 on K<sub>IR</sub>6.1) (Quinn *et al.*, 2004; Shi *et al.*, 2007). Further regulation may occur through dephosphorylation of these residues via the Ca<sup>2+</sup>-dependent phos-

phatase calcineurin (Wilson *et al.*, 2000; Orie *et al.*, 2009). The receptor/PKA/K<sub>ATP</sub> axis may be selectively localized within membrane compartments of the cell. Thus, there is evidence that PKA is largely present in a particulate fashion through interaction with A-kinase anchoring proteins (Hayabuchi *et al.*, 2001a). Furthermore, the channel complex may be localized to caveolae and this may be important for signalling (Sampson *et al.*, 2004; 2007; Davies *et al.*, 2010).

Vasoconstrictors, such as angiotensin II and endothelin-1, activate PKC and there is evidence that K<sub>ATP</sub> channel activity can be modulated through such pathways (Kubo *et al.*, 1997; Cole *et al.*, 2000; Hayabuchi *et al.*, 2001b; Thornehoe *et al.*, 2002; Quinn *et al.*, 2003; Sampson *et al.*, 2007). The regulation is Ca<sup>2+</sup> independent and mediated by PKCε (Hayabuchi *et al.*, 2001b; Quinn *et al.*, 2003). Direct channel phosphorylation of K<sub>IR</sub>6.1 is likely responsible with a cluster of serine residues in the distal C-terminus playing a key role (Quinn *et al.*, 2003; Shi *et al.*, 2008). There may also be effects on channel internalization and recycling perhaps via caveolae (Jiao *et al.*, 2008). Furthermore, vasoconstrictors may inhibit PKA as this would act as an additional inhibitory input to K<sub>ATP</sub> channels (Hayabuchi *et al.*, 2001b). One mechanism that has been little explored is the role of PIP<sub>2</sub> depletion in addition to PKC activation. However, it should be noted that the modulation is essentially abolished by PKC inhibitors and that K<sub>IR</sub>6.1 seems to have a relatively high affinity for PIP<sub>2</sub>, suggesting channel activity may be maintained in the face of substantial depletion (Quinn *et al.*, 2003; Sampson *et al.*, 2007). It should be emphasized that PKC-dependent modulation of VSM K<sub>ATP</sub> channel activity is only likely to account for a part of the action of vasoconstrictors.

A group of endothelial mediators – the so-called gasotransmitters – may also influence VSM K<sub>ATP</sub> channel function (Zhao *et al.*, 2001; Mustafa *et al.*, 2009b). The action of NO is of course well known but the endothelium also generates two other gasotransmitters, CO and H<sub>2</sub>S. H<sub>2</sub>S is produced largely by cystathionine γ-lyase and production is regulated by the activation of Ca<sup>2+</sup>-calmodulin, in a manner analogous to that of NO (Yang *et al.*, 2008). The effector mechanism is thought to be the activation of K<sub>ATP</sub> channels in VSMs through direct modification of channel cysteines, though other mechanisms are possible (Zhao *et al.*, 2001; Cheng *et al.*, 2004; Mustafa *et al.*, 2009a).

Thus, the vascular K<sub>ATP</sub> channel and the cloned equivalent K<sub>IR</sub>6.1/SUR2B are subject to prominent hormonal regulation through direct subunit phosphorylation. What is known about the regulation of K<sub>IR</sub>6.2 complexes particularly in cardiac muscle? This issue is particularly pertinent for PKC modulation as this has been implicated as being central in cellular protection and preconditioning in cardiac cells (Yellon and Downey, 2003). In early studies, PKC modulation was thought to activate sarcolemmal cardiac K<sub>ATP</sub>; however, it now appears that there is a biphasic regulation with activation followed by a slower inhibitory response corresponding to channel internalization (Light *et al.*, 1996; Hu *et al.*, 2003). The phenomena are critically dependent on the prevailing conditions of study. We thought for some time that PKC activation did not modulate K<sub>IR</sub>6.2 (Quinn *et al.*, 2003). However, in intact cells and with higher pipette Ca<sup>2+</sup> in whole cell recordings, we did see biphasic modulation. The inhibitory response was due to channel internalization and



**Figure 2**

Functional roles of K<sub>IR</sub>6.1 and K<sub>IR</sub>6.2 in the cardiovascular system. (A) K<sub>ATP</sub> channels comprising K<sub>IR</sub>6.1 in vascular smooth muscle (VSM) cells regulate vascular tone by controlling the membrane potential and subsequently the influx of Ca<sup>2+</sup> through L-type voltage-dependent Ca<sup>2+</sup> channels. K<sub>ATP</sub> channel activity in VSM can be modulated by the PKC (inhibitory) and PKA (activation) signalling pathways and metabolic stress such as hypoxia and ischaemia. (B) K<sub>IR</sub>6.2-containing K<sub>ATP</sub> channels are predominant in cardiomyocytes, where they are involved in AP repolarization. Activation of K<sub>ATP</sub> by PKC or metabolic insults such as ischaemia and/or hypoxia leads to shortening of AP duration, decreased influx of Ca<sup>2+</sup> and reduced contractility, thus preventing Ca<sup>2+</sup> overload and ATP preservation.

occurred because of phosphorylation of S372 in K<sub>IR</sub>6.2 (Aziz *et al.*, 2012). The regulation of sarcolemmal K<sub>ATP</sub> channels by PKA has been little studied. With K<sub>IR</sub>6.2/SUR1, PKA phosphorylation leads to increased channel activity through residues in SUR1 and K<sub>IR</sub>6.2 that are homologous to those in SUR2B and K<sub>IR</sub>6.1 (Gonoi *et al.*, 1999; Lin *et al.*, 2000; Quinn *et al.*, 2004). Indeed, a plausible *a priori* case could be made for a contribution of sarcolemmal cardiac K<sub>ATP</sub> in the action potential (AP) shortening occurring with the increased heart rate in exercise, in addition to the slowly activating component of the delayed rectifier current. One interesting feature is the subcellular localization of K<sub>ATP</sub> channels that appear to be concentrated at the neck of the T-tubule, suggesting activation could have a significant influence on excitation-contraction coupling (Korchev *et al.*, 2000).

## Pathophysiological function of K<sub>ATP</sub> channels in the cardiovascular system

Generally, three types of study contribute to the understanding of the physiological role of K<sub>ATP</sub> channels: *ex vivo* and *in*

*in vivo* pharmacological studies, functional studies in genetically engineered mice, and human genetics (Figure 2).

### Cardiac protection

Paradoxically, there has been substantial focus on the role of the cardiac sarcolemmal K<sub>ATP</sub> channel in pathobiology (see below), without really addressing the issue of what physiological role the channel might perform in ventricular myocytes. The use of mice with global genetic deletion of K<sub>IR</sub>6.2 (K<sub>IR</sub>6.2 null) has suggested some intriguing possibilities. These animals have an attenuated ability to perform high-intensity exercise and are predisposed to catecholamine cardiotoxicity (Zingman *et al.*, 2002). However, it is not yet clear if it is the deletion in cardiac myocytes that is critical. Channel function will also be impaired in skeletal muscle, pancreatic beta cells and in central neurons, and all of these could have an influence on the integrated physiological function. Mice with cardiac overexpression of a dominant negative K<sub>IR</sub>6.2 subunit had a proarrhythmic phenotype and impaired exercise tolerance (Tong *et al.*, 2006). The study of mice with conditional deletion of K<sub>IR</sub>6.2. (and SUR2) in cardiac myocytes is likely to be highly informative.

Sarcolemmal K<sub>ATP</sub> channels are essentially closed under normal metabolic conditions and hence are thought not to contribute towards the coupling of membrane excitation and contraction in the basal physiological state. In keeping with this, studies in ventricular myocytes from K<sub>IR</sub>6.2 null mice show that AP duration and contractile function are normal (Suzuki *et al.*, 2001). However, exposure to severe metabolic insults such as during hypoxia and ischaemia leads to opening of cardiac K<sub>ATP</sub> channels. Metabolic stress leads to substantial shortening of the AP and attenuated contraction (Lederer *et al.*, 1989; Venkatesh *et al.*, 1991), and these effects are absent when K<sub>IR</sub>6.2 is not present (Li *et al.*, 2000), or in the presence of a K<sub>ATP</sub> channel blocker (Venkatesh *et al.*, 1991). Primarily, opening of K<sub>ATP</sub> channels is likely to be a protective mechanism because the increase in K<sup>+</sup> conductance stabilizes the resting membrane potential, shortens the AP and reduces Ca<sup>2+</sup> influx, resulting in the conservation of intracellular energy stores and preventing calcium overload. In support of this proposal, application of the K<sub>CO</sub> pinacidil enhanced ischaemia-induced AP shortening, early contractile failure and preserved ATP levels (McPherson *et al.*, 1993), and in hearts from K<sub>IR</sub>6.2 null mice, contraction was prolonged and AP duration unaffected during ischaemia (Suzuki *et al.*, 2002). In addition, pinacidil activation of sarcolemmal K<sub>ATP</sub> channels reduced reperfusion-induced Ca<sup>2+</sup> overload in cardiac myocytes, and ablation of K<sub>ATP</sub> channels *in vivo* gives rise to a greater susceptibility to Ca<sup>2+</sup> overload and impairs contractile recovery. Moreover, exercise causes significant remodelling of cardiac K<sub>ATP</sub> channels. Specifically, exercise induces an increase in K<sub>ATP</sub> channel expression (~40%) in mouse ventricles promoting AP shortening in response to an increased heart rate, and these effects are abolished when non-functional K<sub>ATP</sub> channels are transgenically expressed (Zingman *et al.*, 2011). Interestingly, overexpression of SUR2A in cardiac tissue leads to a phenotype protected from ischaemia (Du *et al.*, 2006). An intracellular pool of K<sub>ATP</sub> channels may serve as a reservoir to modulate membrane surface density in stress conditions (Bao *et al.*, 2011a).

There is a substantial body of work proposing that mitoK<sub>ATP</sub> may also have a role in cardioprotection and this has been reviewed in detail elsewhere (Yellon and Downey, 2003). It is worth stating that there are persuasive data favouring the involvement of sarcolemmal cardiac K<sub>ATP</sub> channels in these phenomena, at least in mice. In K<sub>IR</sub>6.2 null mice, the protective effect of ischaemic preconditioning was abolished and recovery of contractile function was compromised (Suzuki *et al.*, 2002; 2003; Gumina *et al.*, 2003). Moreover, the preconditioning effect of diazoxide was also absent (Suzuki *et al.*, 2003).

### Cardiac arrhythmia

The initial opening of K<sub>ATP</sub> channels in response to a metabolic insult is cardioprotective; however, activation of K<sub>ATP</sub> channels also induces early repolarization, thereby shortening the QT interval and reducing the refractory period, hence predisposing to re-entrant arrhythmias. Typical ECG changes observed during ischaemic insults include ST elevation or depression suggesting changes in repolarization. These ischaemia-induced changes in ECG characteristics are ameliorated by the K<sub>ATP</sub> channel blocker glibenclamide and induced by the K<sub>CO</sub> pinacidil (in the absence of ischaemia)

consistent with K<sub>ATP</sub> channel activation underlying these features (Kubota *et al.*, 1993). In support, K<sub>IR</sub>6.2 null mice are not prone to ST elevation in response to ischaemia (Li *et al.*, 2000). However, ischaemia-induced ST elevation was observed in SUR2 null mice (Chutkow *et al.*, 2002). K<sub>IR</sub>6.1 null mice also have episodes of cardiac ischaemia accompanied by ST elevation (Miki *et al.*, 2002). This was originally postulated to be due to the absence of VSM K<sub>ATP</sub> channels; however, it is likely this is not strictly the case as when SUR2B was selectively re-introduced to smooth muscle in SUR2 null mice, the phenotype persisted (Kakkar *et al.*, 2006). These data suggest that K<sub>IR</sub>6.1 in heart may also be involved in early repolarization and ischaemia-induced arrhythmia and is consistent with recent studies showing heterogeneity of K<sub>ATP</sub> subunit composition in different regions of the heart (Flagg *et al.*, 2008; Bao *et al.*, 2011b). Early repolarization patterns in the ECG has historically been considered to be of little consequence and is commonly observed in healthy males and athletes. However, there is now evidence to suggest that the early repolarization pattern ('J wave syndromes') may be associated with increased risk of ventricular fibrillation (Antzelevitch, 2012). A clear association of K<sub>ATP</sub> channels with early repolarization syndromes was made when Haissaguerre *et al.* (2009) found a rare variant of KCNJ8 (K<sub>IR</sub>6.1) in a patient with idiopathic ventricular fibrillation and prominent early repolarization. In further independent studies, the same missense mutation of a highly conserved serine to leucine (S422L) was discovered in five more patients (Medeiros-Domingo *et al.*, 2010; Barajas-Martinez *et al.*, 2012). Both studies showed an increased current density when K<sub>IR</sub>6.1-S422L was co-expressed heterologously with SUR2A. Mechanistically, this gain of function in the mutant channel can be explained by the decreased ATP sensitivity of K<sub>IR</sub>6.1-S422L channels compared with wild-type (WT) channels (Barajas-Martinez *et al.*, 2012).

Most studies of cardiac arrhythmias resulting from myocardial ischaemia have been focused predominantly on the abnormalities of ventricular rhythm and relatively little is known about the role of K<sub>ATP</sub> channels in abnormal atrial rhythm. A recent study has shown that activation of K<sub>ATP</sub> channels by  $\beta$ -adrenoceptor-induced metabolic stress provides a substrate for atrial tachyarrhythmias in mouse isolated heart (Kim *et al.*, 2012). In support, pinacidil shortens atrial AP duration and increases arrhythmia inducibility in human right atrial and right ventricular wall (Fedorov *et al.*, 2011). Furthermore, atrial electrical remodelling and increased arrhythmia inducibility in a murine model of salt-induced hypertension have been shown to be associated with increased K<sub>ATP</sub> current and SUR1 expression (Lader *et al.*, 2011). A recent screening of patients with atrial fibrillation found two patients with the K<sub>IR</sub>6.1-S422L variant (Delaney *et al.*, 2012).

### Heart failure, hypertrophy and cell swelling

Cardiac hypertrophy is triggered by a prolonged increase in cardiac workload. When transverse aortic constriction was applied in K<sub>IR</sub>6.2 null mice or in mice with cardiac specific overexpression of SUR1 which paradoxically disrupts cardiac sarcolemmal K<sub>ATP</sub> channel function, increased left ventricular hypertrophy was observed (Yamada *et al.*, 2006; Hu *et al.*, 2008). Interestingly, there seems to be an interaction between

cardiac  $K_{ATP}$  channel expression and the activity of the PPAR- $\gamma$  coactivator, PGC-1 $\alpha$ . Decreased channel function leads to decreased activity at the PGC-1 $\alpha$  promoter partly via FOXO-1 repression (Hu *et al.*, 2008). Remodelled ventricular cardiomyocytes from rats subjected to coronary occlusion show up-regulation of  $K_{IR6.1}$ , especially around the infarct zone (Isidoro *et al.*, 2007). Congestive heart failure or infarction in human hearts leads to an increased AP duration and sensitivity to potassium channel openers in both atria and ventricles (Fedorov *et al.*, 2011). There are a variety of other molecules/enzymes that have been shown to be involved in the progression from compensated hypertrophy to heart failure possibly by their interactions with  $K_{ATP}$  channels. Angiotensin II and TNF- $\alpha$  expression is positively correlated to that of  $K_{IR6.1}$  in failing rat myocardium or cultured cardiomyocytes and negatively correlated with  $K_{IR6.2}$  (Isidoro *et al.*, 2009). Furthermore, cardiomyocytes treated with these were responsive to diazoxide, indicating increased expression of  $K_{IR6.1}$ /SUR2B in these cells as part of the progression to hypertrophy (Isidoro *et al.*, 2007; 2009).

Various mutations have been identified within  $K_{ATP}$  channel subunits which confer susceptibility to cardiomyopathy, hypertrophy and heart failure. A cohort of patients with dilated cardiomyopathy allowed the identification of a frameshift mutation leading to a premature stop codon at Leu1524 and a missense mutation A1513T in SUR2A. Both mutations are located in the NBD2 and compromise the ability of ATP to be hydrolysed (Bienengraeber *et al.*, 2004). In  $K_{IR6.2}$ , a non-synonymous polymorphism leading to the coding change, E23K, was identified in 18% of heart failure patients (Reyes *et al.*, 2009) and is also known to lead to an increased risk of type 2 diabetes (Gloyn *et al.*, 2003). Both heterozygous and homozygous patients have the same resting heart rates and show similar degrees of left ventricular dysfunction and remodelling. When these homozygous patients are exercised, they show a reduced heart rate, oxygen consumption and peak  $VO_2$ . Other missense mutations in SUR2A within transmembrane domains have also been identified to cause activation of the channel in the rare Cantu syndrome, characterised by cardiac hypertrophy and cardiomegaly (Harakalova *et al.*, 2012). Although the human and murine experimental data are very different in nature, there seems to be inconsistency in that both reduction and increases in  $K_{ATP}$  channel activity, can result in cardiac hypertrophy.

Excessive changes in cell volume in the heart can result in the alteration of the structural integrity of the cells affecting cellular functions and cell death. These changes can arise as a result of an intracellular accumulation of metabolites that increase cellular osmolality, allow water to enter the cell, increase the cell volume and alter ion channel function. Reduction of cardiomyocyte swelling during myocardial ischaemia may be a potential mechanism of cardioprotection (Shi *et al.*, 2009).  $K_{ATP}$  has been shown to be regulated during cell volume changes with atrial  $K_{ATP}$  channels opening in response to cell swelling leading to AP shortening (Saegusa *et al.*, 2005). The absence of  $K_{IR6.2}$  in cardiac myocytes isolated from  $K_{IR6.2}$  null mice prevents cell swelling from occurring whereas in WT mice there is exaggerated cell swelling which can be disrupted by the addition of diazoxide (Prasad *et al.*, 2006). The use of diazoxide in some of the studies

appears to be more complicated. Although cell swelling could be diminished by the addition of diazoxide, the addition of HMR1098 and 5-hydroxydecanoate did not reverse the events initially suggesting that diazoxide may be acting via a mechanism separate from the activation of  $K_{ATP}$  channels (Maffit *et al.*, 2012).

### Vascular reactivity and hypertension

The modulation of VSM  $K_{ATP}$  currents by vasoactive agents suggests the channel may be important for blood pressure control. In VSM cells from  $K_{IR6.1}$  and SUR2 null mice  $K_{ATP}$  currents were absent, whereas cells from  $K_{IR6.2}$  null mice exhibited normal  $K_{ATP}$  currents (Suzuki *et al.*, 2001; Chutkow *et al.*, 2002; Miki *et al.*, 2002). As well as providing direct evidence for the molecular composition of the VSM  $K_{ATP}$  channel,  $K_{IR6.1}$  and SUR2 null mice exhibit hypercontractility of the coronary vasculature and are prone to early sudden death due to coronary artery spasm (Chutkow *et al.*, 2002; Miki *et al.*, 2002). SUR2 null mice also show focal narrowing of the coronary arteries and have significantly elevated blood pressure (Chutkow *et al.*, 2002). Interestingly, restoration of the vascular  $K_{ATP}$  channel in SUR2 null mice does not protect against a rise in baseline coronary artery perfusion pressure suggesting a role for  $K_{ATP}$  channels from tissues other than VSM (Kakkar *et al.*, 2006). Specifically, SUR2B RNA has been detected in endothelium and it is believed that heteromeric  $K_{IR6.1}$ / $K_{IR6.2}$  in combination with SUR2B could form an endothelial  $K_{ATP}$  channel (Yoshida *et al.*, 2004). In mice expressing endothelium-specific dominant-negative  $K_{IR6.1}$  subunits, basal coronary perfusion pressure and ET-1 concentrations were substantially elevated suggesting a role for endothelial  $K_{ATP}$  channels in the regulation of vascular tone (Malester *et al.*, 2007).

Further evidence for the role of VSM  $K_{ATP}$  channels in vascular tone regulation comes from studies of hypertensive animal models where there is substantial remodelling of  $K_{ATP}$  channels in vascular beds (Blanco-Rivero *et al.*, 2008; Tajada *et al.*, 2012).  $K_{ATP}$  channels in hypertensive phenotypes show altered vascular reactivity probably as a result of impaired and fewer  $K_{ATP}$  channels. VSM cells from hypertensive animals are significantly depolarized and  $K_{CO}$  compounds have little effect on membrane potential compared with normotensive animals (Tajada *et al.*, 2012). The  $K_{CO}$  iptakalim has been put forward as a promising anti-hypertensive agent for mild to moderate essential hypertension (Sikka *et al.*, 2012). Interestingly, on a mechanistic level iptakalim has also been shown to inhibit ET-1 release and synthesis and increase NO release and NOS activity in aortic endothelial cells (Gao *et al.*, 2009). Additionally, there are data to suggest that  $K_{CO}$  compounds such as iptakalim have therapeutic potential as a treatment for pulmonary hypertension (Sikka *et al.*, 2012).

### Sepsis

The role of  $K_{ATP}$  channels in sepsis is complex (Buckley *et al.*, 2006). There is pharmacological evidence that channel activation occurs in septic shock leading to hypotension and this can be reversed by glibenclamide (Matsuda and Hattori, 2007). There is also evidence for increased activity of these channels but that their pharmacology alters such that they become unresponsive to sulphonylureas and only direct

pore blockers can inhibit activity (O'Brien *et al.*, 2009), and this is consistent with the lack of clinical efficacy (Warrillow *et al.*, 2006; Morelli *et al.*, 2007). However, animals, and also flies, with global genetic deletion of the channel are predisposed to an early and substantial survival disadvantage in sepsis (Kane *et al.*, 2006; Croker *et al.*, 2007). Furthermore, the expression of K<sub>IR</sub>6.1 is regulated via Toll-like receptors and NF-κB and the increase in expression of the current is postulated to underlie the poor response to vasoconstrictors in septic shock (Shi *et al.*, 2010). The exact mechanism for the survival disadvantage is unclear but inappropriate coronary artery vasoconstriction during increased cardiac demand is one proposal. However, the pathophysiological circulatory changes in severe sepsis are actually profound and widespread. These include hypotension, hyporesponsiveness to vasoconstrictors, microvascular dysfunction, endothelial dysfunction, and increased vascular and capillary permeability (Matsuda and Hattori, 2007). The absence of K<sub>IR</sub>6.1 in both smooth muscle and endothelium may promote these adaptations.

## Conclusions

The physiological role of K<sub>ATP</sub> channels is well defined in the pancreatic beta cell. Recent work has begun to reveal similar pathophysiological importance in the function of cardiac muscle, specialized conduction tissues in the heart and of VSM (Figure 2). These channels have a rich existing pharmacology that could be exploited to develop novel therapeutic agents for the treatment of cardiovascular disease.

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## Conflict of interest

The authors have no conflicts of interest to declare.

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